

FIG. 1

*FIG. 2a*

~~FIG. 2~~

GGT GAA GAA GGA GTT GTG CCA GCA CGT GAG TAC TCA GAC GAT CGT 45  
Gly Glu Glu Gly Val Val Pro Ala Arg Glu Tyr Ser Asp Asp Arg [15]

AAC ATC AAC CTG GCA GAC GAA TTA AAA ATT GGT GAT ACC ATT GAA 90  
Asn Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu [30]

GCA GTT GTC ATT TCT AAC GTA ACA AGC GAC AAG GAA GGC GTC AGT 135  
Ala Val Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser [45]

TAC TTG TTG TCA AAG AAG CGT TTG GAT GCG CGC AAG GCA TGG GAA 180  
Tyr Leu Leu Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu [60]

AAC TTG AGC TTT GCT GAA GGT GAC ACA GTT GAT GCC AAG GTT ATC 225  
Asn Leu Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile [75]

AAC GCT GTT CGT GGT TTG ATT GTT GAT GTT AAC GGC GTA CGT 270  
Asn Ala Val Arg Gly Leu Ile Val Asp Val Asn Gly Val Arg [90]

GGT TTC GTA CCA GCA TCA ATG GTT GCA GAA CGT TTC GTT TCT GAT 315  
Gly Phe Val Pro Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp [105]

TTG AAC CAA TTC AAG AAT AAG GAT ATT AAA GCA CAA GTT ATC GAA 360  
Leu Asn Gln Phe Lys Asn Lys Asp Ile Lys Ala Gln Val Ile Glu [120]

ATT GAC CCT GCT AAT GCA CGT TTG ATT TTG TCA CGT AAG GCT GTT 405  
Ile Asp Pro Ala Asn Ala Arg Leu Ile Leu Ser Arg Lys Ala Val [135]

GCT GCA CAA GAA CGC GCT GCA CGA TTG GCT GAA GTA TTT AGC AAG 450  
Ala Ala Gln Glu Arg Ala Ala Gln Leu Ala Glu Val Phe Ser Lys [150]

TTG TCA GTT CGT GAA GTT GTT GAA GGA ACT GTT GCC CGT TTG ACA 495  
Leu Ser Val Gly Glu Val Val Glu Gly Thr Val Ala Arg Leu Thr [165]

GAC TTC GGC GCA TTC GTT GAC TTG GGT GGT GTT GAT GGT TTG GTT 540  
Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val Asp Gly Leu Val [180]

CAC GTA TCA GAA ATC TCA CAC GAT CGT GTG AAG AAC CCG GCC GAT 585  
His Val Ser Glu Ile Ser His Asp Arg Val Lys Asn Pro Ala Asp [195]

GTA TTG ACA AAG GGT GAC AAG GTT GAT GTT AAG ATC TTG GCA TTG 630  
Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys Ile Leu Ala Leu [210]

GAC ACT GAA AAG GGT CGT ATC TCA TTG TCA ATC AAA GCA ACA CAA 675  
Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys Ala Thr Gln [225]

FIG. 26

~~FIG. 26~~

CGT GGA CCT TGG GAC GAA GCT GCA GAT CAA ATC GCT GCA GGT TCA 720  
Arg Gly Pro Trp Asp Glu Ala Ala Asp Glu Ile Ala Ala Gly Ser [240]

GTG CTT GAA GGT ACT GTT AAG CGT GTG AAG GAC TTT GGT GCC TTT 765  
Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Glu Ala Phe [255]

GTT GAA ATT TTG CCT GGT ATC GAA GGT CTT GTG CAC GTG TCA CAA 810  
Val Glu Ile Leu Pro Glu Ile Glu Gly Leu Val His Val Ser Glu [270]

ATT TCA AAC AAG CGT ATT GAA AAC CCA TCA GAA GTT TTG AAG TCT 855  
Ile Ser Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser [285]

GGT GAC AAG GTA CAA GTG AAG GTA TTG GAC ATT AAG CCA GCC GAA 900  
Gly Asp Lys Val Glu Val Lys Val Leu Asp Ile Lys Pro Ala Glu [300]

GAA CGT ATT TCA TTG TCA ATG AAG GCT TTG GAA GAA AAG CCA GAA 945  
Glu Arg Ile Ser Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu [315]

CGT GAA GAT CGT CGT GGT AAC GAT GGT TCA GCT TCA CGT GCT GAT 990  
Arg Glu Asp Arg Arg Gly Asn Asp Glu Ser Ala Ser Arg Ala Asp [330]

ATC GCT GCT TAC AAG CAA CAA GAT GAC TCA GCC GCA ACA TTG GGT 1035  
Ile Ala Ala Tyr Lys Glu Glu Asp Asp Ser Ala Ala Thr Leu Gly [345]

GAC ATC TTT GGT GAT AAG TTG TAA GAGGCATCACATAAAAGAGCTGGTTC 1086  
Asp Ile Phe Glu Asp Lys Leu \*\*\* [352]

GCCAGTTCTTTATTTTGAAGAAAAATTGAGTGGGCATTAGTGGCGCTACGGTATG 1145

AAAAAGGAGGTGCGATTATGGCAGCACCAGTAGTAGCCATTGTTGGCGACCAAACGTCG 1204

GAAAATCGACTATCTTAACCGGATGGCCGGAGAACGTATTGCAATTGTTGAAGATCAA 1263

CCAGGGGTAACACCGCGATCGTTGTACCGGCCAGCCGAATGGTTGAATTAT 1314

~~FIG. 3a.~~ ~~FIG. 3~~

|     |     |  |       |
|-----|-----|--|-------|
| HS1 | 63  | SFAEGDTVDAKVINAVRGGLIVDNGVRGFFVPASMV/AERFVSDLNQFKNNDIKAQVIEI               | 121   |
| ES1 | 101 | AYEDAE - TGVINGK-K - FT-ELD - I - A-L - G- L - DV-P-R -TLEFK-- KL          | 159   |
| RS1 | 107 | K- EA- ER- EGIIF- Q-K --FT- -LD- AVA -L -R-Q - DI -P/R -VTPADAQPAAALRNLM   | 165   |
| PS1 | 1   | E- -TGVINGK-K -FT- EL- -I - A - L -G-L - DV-P-R-TTHLEG -ELEFK -- KL        | 54    |
| CS1 | 182 | -DW-KG- IVG-NK- -W/AL-E -L- - - -F-Q- ISSK -SAEELLE - E-PLKFV - V          | 236   |
|     |     | a b c  | ***   |
|     |     | ****   | ***** |
| HS1 | 122 | DPANARLILSRKAVAAQERAQALAEVFSKLSVGGEVWEGTVARLTDFFGAFVDLGGVDGLV              | 180   |
| ES1 | 160 | -QKRNNWW--R- -IES - NS- ERDQLLEN-QE- ME-K- I -KN- -Y- - - - -L             | 21    |
| RS1 | 166 | -KRRGNWW --RT -LEES - -E - RS-IVQN -EE- Q- - -V -KNI - -Y- - - - -L        | 22    |
| PS1 | 55  | -QKRNNWW--R- -IES - SS- ERDQLLEN -QE- ME-K- I -KN- -Y- - - - -L            | 11    |
| CS1 | 237 | -EEQS--VM-NRKAM-DSQ- M- DSQAQ-GI- S - -T- - -QS-KPY- - -I - - -N - -L      | 28    |
|     |     | d e  | ***** |
|     |     | ****   | ***** |
| HS1 | 181 | HVSEISHDRVKNPADVLTKGDKVUDKILADTEKGRISLSIKATQRGPWDEADQIAAG                  | 23    |
| ES1 | 219 | -ITDMAWK-- -H-SEIVNV - -E IT - -V -KF-R- RT -V - -GL -QLGED- -VAI - KRYPE- | 27    |
| RS1 | 225 | -ITDMAWR-- -H-SEIQNI - -QQ-K- Q- IRINQ- TH - - -GM -QLESD--GIGAKYPV-       | 28    |
| PS1 | 114 | -ITDMAWK-- -H-SEIVNV-- E IT - -V -KF-R- RT -V - -GL -QLGED- -VAI - KRYPE-  | 17    |
| CS1 | 288 | -Q - - - -SDI - T--QP- - TLK - M--SH-R- R- -V - - -T-KLEPT - G-            | 33    |
|     |     | a b c  | ***** |

FIG. 36

|       |   |     |
|-------|---|-----|
| HS1   | 240 SVLEGTIVKRVKDFGAFVEILPGIEGLVHVSQISNIKRIENPSEVLKSGDKVQVKVLDIKP | 298 |
| ES1   | 278 TK-T-R-TNLT-Y-C---EE-V------EM RD-V-DATL--SV--E- EA-FTGVDR    | 510 |
| RS1   | 284 KK\$---TNT-Y------LE-----I-EM -RPG-QVH-EFNK--V- RAV--vDV      | 430 |
| PS1   | 173 TK-T-R-TNLT-Y-C---EE-V------EM -K-- E IAAV -- QVDA            | 319 |
| ***** |   |     |
| e     |   |     |

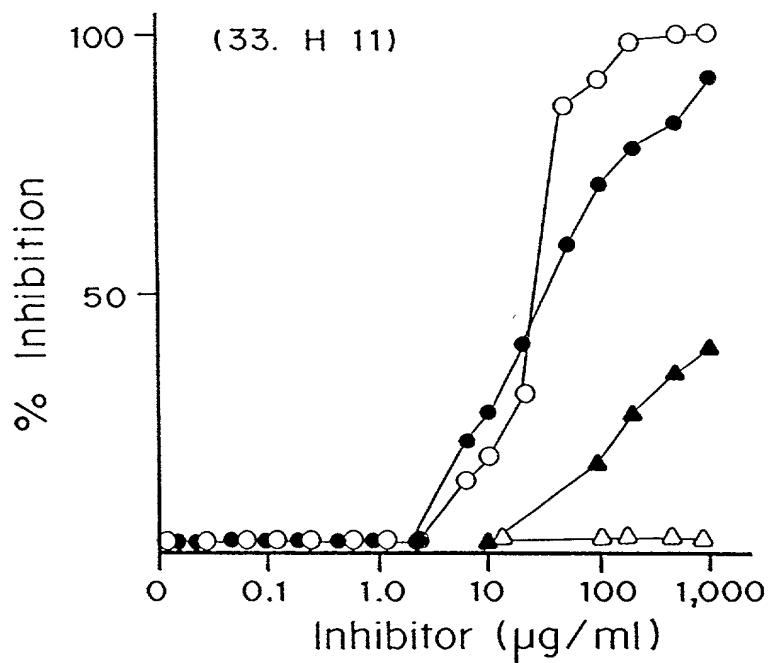


FIG. 4a

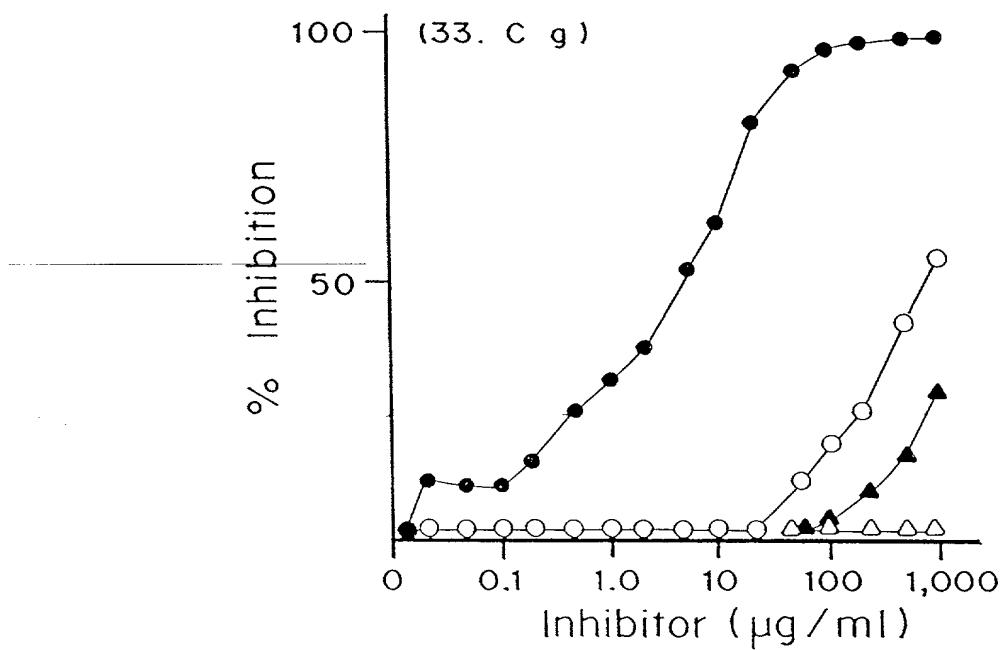


FIG. 4b

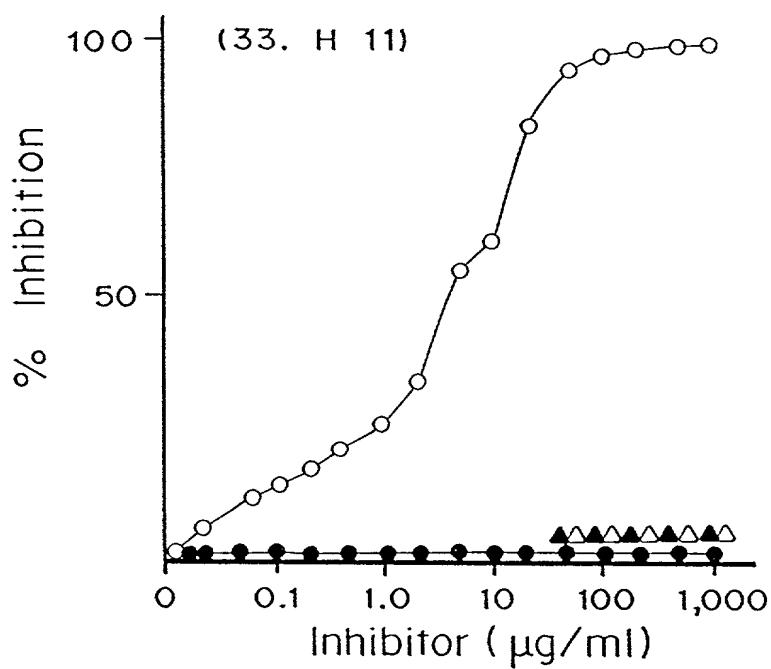


FIG. 4c

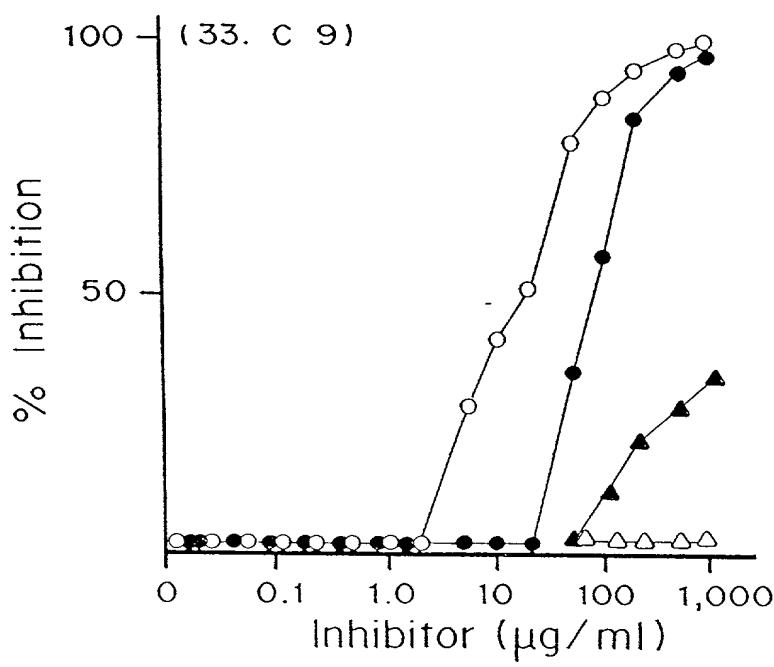


FIG. 4d